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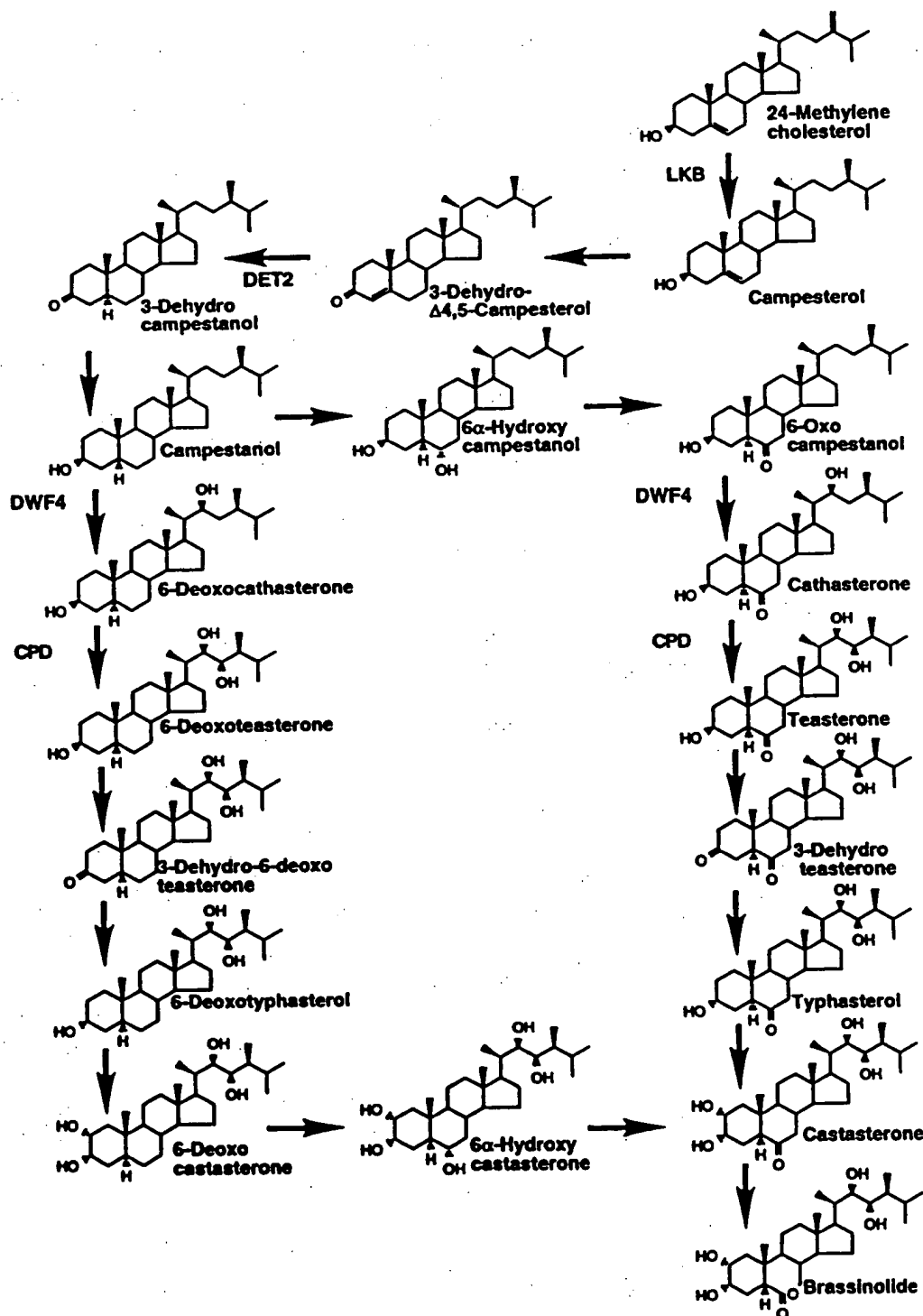
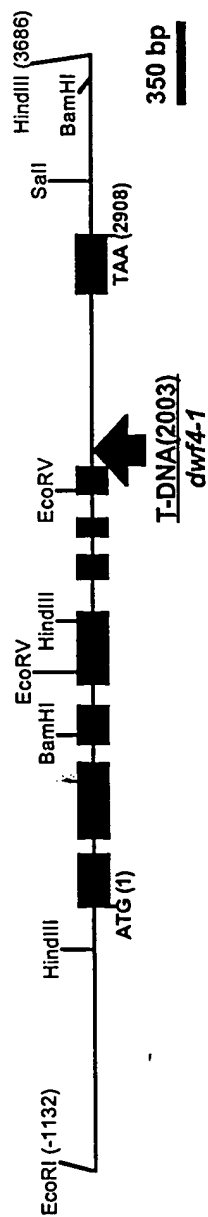


FIG. 1

A) *DWF4* locus



B) Domains and Mutations

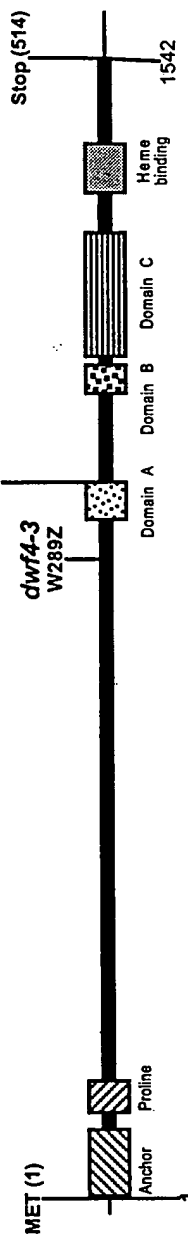


FIG. 2



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DWF4<CYP90B>
CPD<CYP90A>
Tomato<CYP85>
Cyanobacteria<CYP120>
Maize<CYP88>
Zebrafish<CYP26>
Human<CYP3A3X>
CONSENSUS

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1      10      20      30      40      50      60      70
... M F E T E H H T L L P L L L ... P S I L L S L L L F L L L L K K A R N ... R K ... T R F
... M A F I ... A F L L ... L S S I A A G ... F L L L L R A T ... R Y ... R A M
... M A F F ... L I F ... S S F F G L C I F C T A L L A W N Q V K Y ... M I T S P I T N L N S L ... N O K
... M L G V G M A A A V L L G A V A L L L A D A A A R R A H W W Y R E A A E A V ... V G A V A ... V V V D A A A A R A H G W Y R E A A L G A A R A
... M G L Y T L M V T F L C T I V L P V L P L A A V K L W E M L M I R R V D P N C B S
... M A I P D L A M E T W L L A V S L V L L Y L V G T H S H G L F K K
... I L G A L Y I L A A R ... r y ... r r k
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ANCHOR REGION

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80      90      100     110     120     130     140     150
N P P C K S G W P F L G E T I G Y L K P Y T A T T L G D M Q O H V S K Y G ... K I Y R S N L F G E P T I V S A D A G L N R F I L O M E G R L F E C S Y P S T G G I
G L P D G G S L G L I G E T F Q L I G A Y K T E N P E P I D E R V A R Y G ... S V F M T H L F G E P T I F S A O P E T N R F V L O M E G K L F E C S Y P S I C N L
N P D D G G I M G W P L F G E T T E F L K L ... G P S E M K N O R A R Y G ... S F F K S H L G C P T V S M O S E L N R Y I L V N E A K G L V P G Y P S M I D I
P L D D G G E G L P W L G E T L N F ... L N D G D G K K R Q O O F G ... P I F K T R L F G K N V I F S G A L A N R F L E T K E O E T F O A T W P L S T R I L
R L D D G G M G W P L V G G M W A F L R A F K S G K P D A I A S F V R R F G R T ... G V R S F M F S S P T V L V T T A E G C K O V L M D D D ... A F V T G W P K A T V A L
L G I P G G T P L P F L G N I L S Y H K G F C M ... L O R R K E L R M K R O K Y G ... C I Y K T H L F G N P T V R V M G A D N V R O I L V G E H K L V S V Q W P A S V R T
... P G I M A L P I G E T I q i k ... p g d ... k e r v ... y g ... i y k h i f g e p t i ... s d a e l n r i l i n e g k i l c ... P a s ... g
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PROLINE

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160     170     180     190     200     210     220     230     240
L G K W S M V L V G D M R D M R S I S L N F L S H A R L R T I L K D V E R H T L F I V L D S W ... Q Q N S I F S A O D E A K F I F N L M A R H I M S M D P G E E
L G K H S L L M K G S L A K R M H S L T M S I A N S S I K D H L M L D K D M R F H L D S W ... S S R V L L M E E A K F I F E L T V K O L M S F D P G E W
L G K C N I A A V N G S A K Y M R M G A L L S L S P T M I R D O L P K I D E F M R S H L T N W ... D N K V I L D I Q E T N M A F I F E L T V K O L M S F D P G E W
L G P N A L A T O M G E I H R S R R K I L Y Q A F L P R T L D S Y L P K M D G I V O G Y E O W ... G K A N E W Y P O L R M E F D V A A T L F M G ... E K V
V G P R S F A M P Y D E H R R I R K L T A A P I N G F D A L T G Y L P O R T V T S S R A W ... A D H G G S V E L T L R R M E F K I I V O I F L G G A D O A T
G S D T L S N V H G V O A K N K K K A I M R A F S R D A L E H Y I V O E M K S A I O E W ... L O K D S C V L V P E M K K L M A R I A M R I L L G F E P E Q I K
M K S A I S I A E D E E W A R L S L S P T F T S G K L K E M V A I A Q Y G D V L R N L R R E R E T G K P I T L K D V F G A Y S M D V I T S S S F G V N V D S L N
l g k s l a a g e h k r m r l l s l s ... i d h l p i d r v r s l ... w ... q k ... i v ... e k k m l f d ... k ... m g ... p ... e
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250     260     270     280     290     300     310     320
T E ... O L K E Y V T F M K G V V S A P L N L P G T A Y H K A L G S R A T I L K F I E R A M E R K L D I K E E D O E E E V K T I E D E A E M S K S D H V R K O R T D D
S E ... S I R K E Y L L V I E G F F S L P L P L F S T T V R K A I Q A R ... R A V A L E A L T V V M K R R E E ... E E G A E ... R A K K D M
A O ... E F M S E F F N L V L G T I L S L P I N L P N T I L H R G F O A R K I I V N L R ... T L I E E R A S K E I ... E E G A E ... Q H D
S O N P O F P W F E T Y I O G L F S L P I P L P N T L F G K S O R A R A L L A E L E K I I K A R ... Q Q O P S E E ... D A
T R ... A L E R S Y T E L N Y G M R A M A I N L P G F A R G A L R A R R L V A V L O ... G V L D E R A A R A K G V S G G G V ... O K Y K D A
T D E O E V E A F A E M I K N L F S L P I D V P F S G L Y R G L R A R N F I H S K I E N I R K K ... I O D D N E N E ... O K Y K D A
N P O D P I V E N T K K L R F D F L D P F L S I I V F ... P F L I P I L E ... V L N I C V F P R E V N F L R A V K R M K E S R L E D T O K H R V D
l ... l v e e l i k g l i s i p i n l p t a y k a l a r a f a l e ... i e r e e e ...
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330     340     350     360     370     380     390     400     410
I L G W V L K ... H S N ... L S T E O L D L I L S L F E A G H E T S S V A I A L A I F F L Q A C P K A V E E L R E E M L E A R A K K E L G E S E L N W D Y
I L A A L A A ... D D G ... F S D E E I V D F L V A L L V A G Y E T I S T I M T L A V K F L T E T P L A L A O L K E E K E I ... R A M K S D S Y S L E W S D Y
M L G Y L M N ... E E A T R F K L I D D E M I D L I I T I L Y S G Y E T I S T S M M A V K Y L H D H P K V L E E L R K E H M A L R E K K K P E D P I D Y N D Y
G I L A A ... R D D N N O P L S I P E L K D O I L L E A G A E L T S A L S S E C L L G O H S D I R E R V R O E O N K L O L ... S Q E L T A E T L
M D R I E A ... O D E R G R H L D D E I I O V L V M Y M A G H E S S G H I T M W A T V M F L G E N D P M F A R A K A E Q E A Q E K V E M G M Y T P G K G S M E L L
Q O L I E N ... S R R S D E P E S L O A M K E A A T L F E G G H E T A T A S T S L V M E L G N T E V V O K V R E E V O E K V E M G M Y T P G K G S M E L L
F L O M I D S H K N S K E T E S H K A L S O L E L V A Q S I I F I A G Y E T I S S V L S I M Y E L A T H P D V O O K L Q E I D A V L P N K ... A P P T Y D T V
l i g i l a ... e d e ... l s d e i d i ... l i l a g h e t i s s l ... a x k l e h p d v e l r e e h a i r a k k ... e s l l d y
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Domain A

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420     430     440     450     460     470     480     490     500
K K M D F T O C V I M E T L A L G M V I R F L H A K A L K D V R Y K G Y O I P S G W A V L P V I S A V H L O N S R Y D O P N L F M P H A R G Q O N N G A S S G S G S F S T
K S M P F T O C V I M E T L A L G M V I R F L H A K A L K D V R Y K G Y O I P S G W A V L P V I S A V H L O P N H F K O A R T F M P H A R G Q O N N G A S S G S G S F S T
R S M R F T R A V I L E T S R L A T I V N G V I R K T T O D M E I N G Y I P K G W R I Y V V T R E L Y O P D L Y P O P Y S A N N P H A R G Q O N N G A S S G S G S F S T
K K M P Y L D O V L O E V L R L I P P V G G G F R E L I O O C O F O G F H P K G W A V L P V I S A V H L O P N H F K O A R T F M P H A R G Q O N N G A S S G S G S F S T
R K M E V L S O V I D E T L R L N P P V G G G F R E L I O O C O F O G F H P K G W A V L P V I S A V H L O P N H F K O A R T F M P H A R G Q O N N G A S S G S G S F S T
D O L K M G V I K E T L R L N P P V G G G F R E L I O O C O F O G F H P K G W A V L P V I S A V H L O P N H F K O A R T F M P H A R G Q O N N G A S S G S G S F S T
L O M E L O M V N E L R L F P M A M R L E R V C K K D V E L N G M F I P K G W A V L P V I S A V H L O P N H F K O A R T F M P H A R G Q O N N G A S S G S G S F S T
k k m y i c v i n e t i r i a l v g g f r a k d v e l n g y l p k g w k y y s i r a v h l d d v p d e k e n p r w ... k ... s n s
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Domain B

Domain C

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510     520     530     540     550     560     570
W G M N Y M P F G G G P R L C A G S E L A K L E M A V F I H H L V L K E N E L A E D D ... O P F A F F F V D F P N G L P I R V S R I L ...
... M V F T P F G G G P R L C P G Y E L A R V A L S V F L H R L Y T G A S W P E A L E O D ... K V F F F A T T R T O K R Y P I F V K I R D F A T ...
... F L V F G G G P R L C P G Y E L A R V A L S V F L H R L Y T G A S W P E A L E O D ... K L M K F P R V E A P N G L R I R V S A H ...
... A H V F G G G P R L C P G Y E L A R V A L S V F L H R L Y T G A S W P E A L E O D ... E L V V T P S P R P K D N L R V K L H S L M ...
R A G T F L A F G G G P R L C P G Y E L A R V A L S V F L H R L Y T G A S W P E A L E O D ... R V R Y L P H P R P V D N C L A K I T R V G S ...
... N Y I P F G G G P R L C P G Y E L A R V A L S V F L H R L Y T G A S W P E A L E O D ... T M K T G A T I Y P V D N L P T K E T S Y V R N ...
... Y I Y T P F G G G P R L C P G Y E L A R V A L S V F L H R L Y T G A S W P E A L E O D ... P L K S L G G L L O P E K P V V L K V E S R D G T V S G A
... n ... P F G G G P R L C P G Y E L A R V A L S V F L H R L Y T G A S W P E A L E O D ... k l v l p l r p d n l p i k v r d ...
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HEME-BINDING

FIG. 3

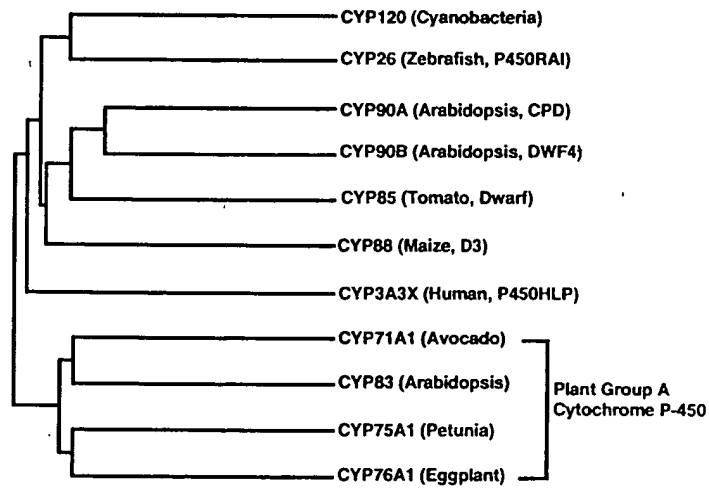


FIG. 4

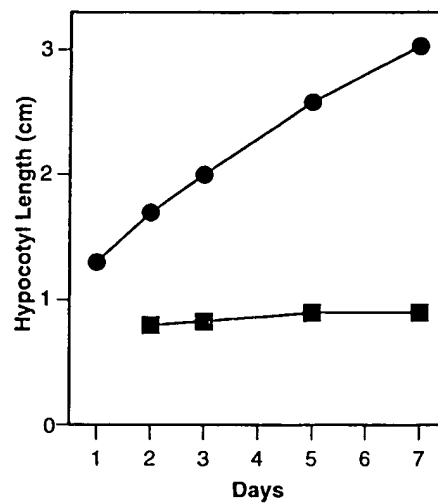


FIG. 5

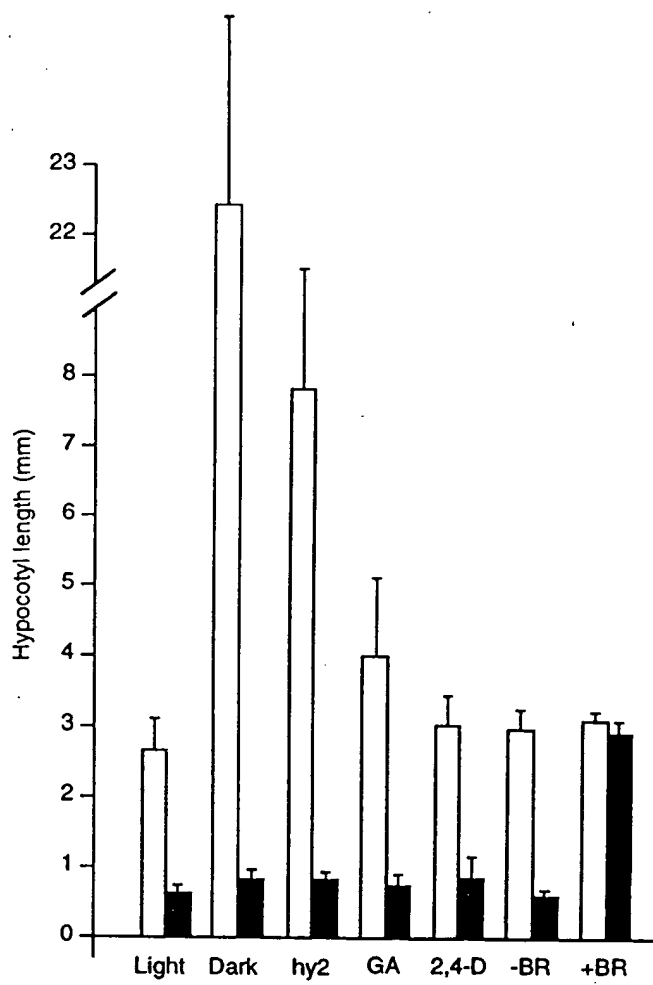


FIG. 6

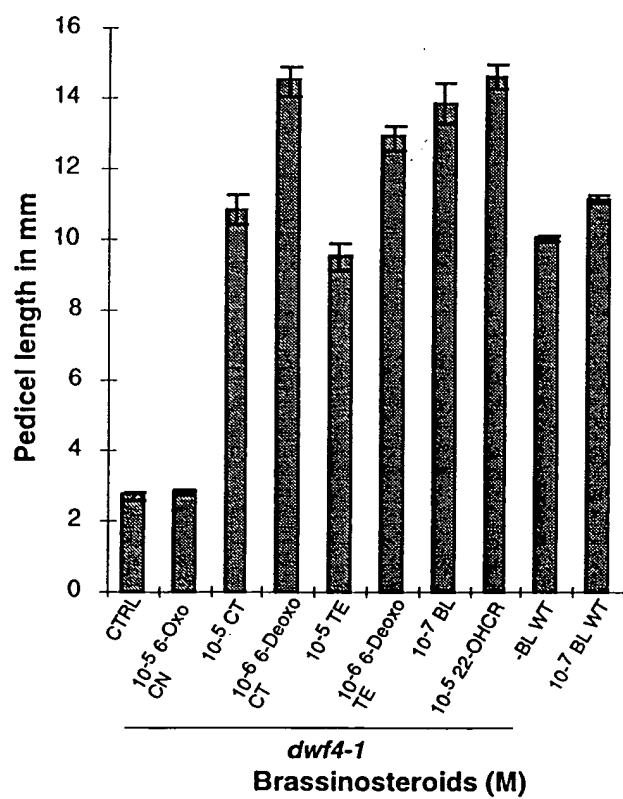


FIG. 7

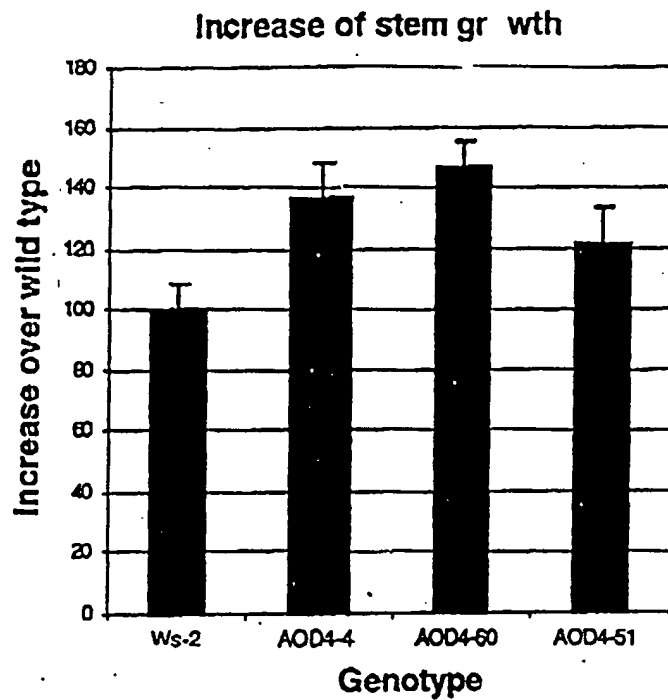
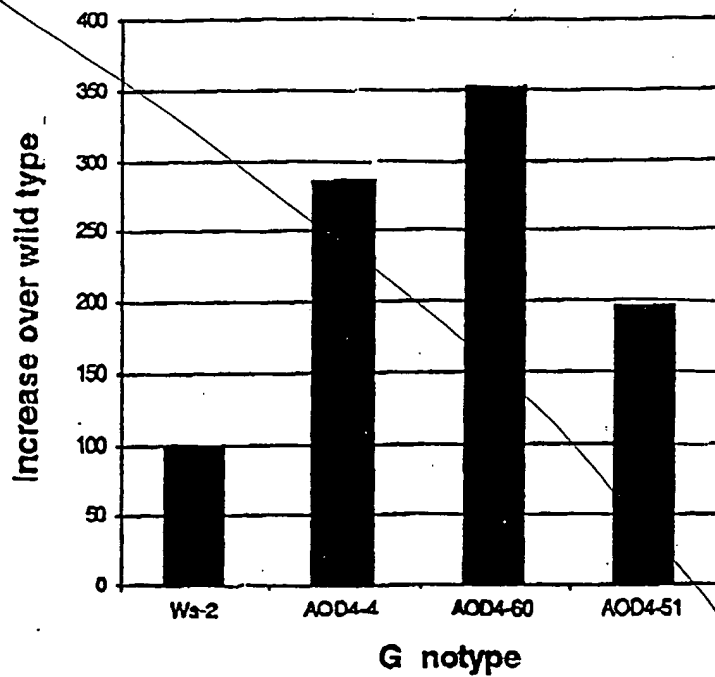


FIG. 8

Increased seed production due to DWF4 overexpression



Cancelled and
replaced with substitute
figure 9, submitted
03/07/03.

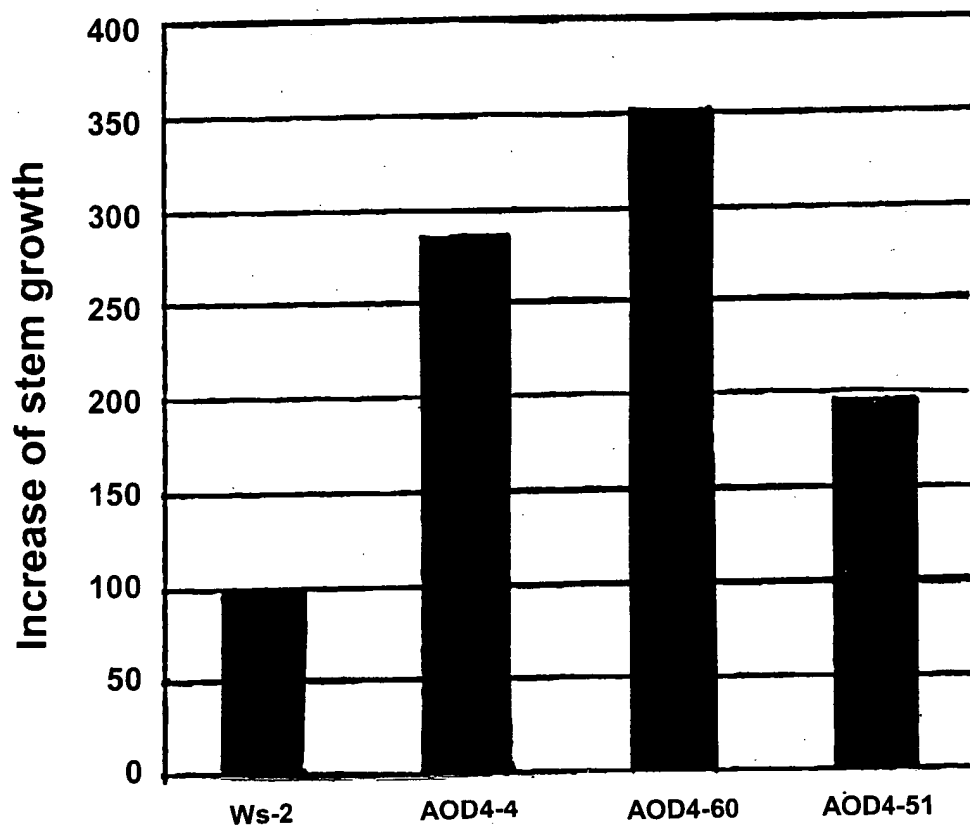
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FIG. 9



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Increased seed production due to DWF4 overexpression



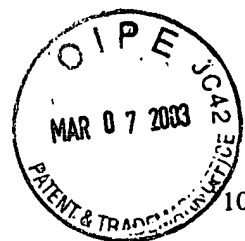
Genotype

FIG. 9



1 ATGTGGGTATTATATTGTTGGGTTCGGTTTGAGCTACAATATAAAATTCGTGTTTCTGGT 60
61 TATTCTGTTACATGATTTGAGTTTGGTTCTCAATTTGGATTCCAAGATAATTAAATATT 120
121 AAAATTCATTTAAAATATTTACAAGTAATTAATTATCTTTACATTGTATTGTTATAACAA 180
181 AATATCTATCTTTGGTATATGAGAAAAATATGGAGTTTGAATTATAATAATAAGGAAA 240
241 TAATCGATTCCATTTGGTTGGATTACACAGTTAAGTTTTTGTGTTTCTTTTGTATATGT 300
301 ATATGAGTAAATCAAAAAGAGTATTGATTGAAGTGTAACATATTCGTTATGACCCCCA 360
361 AAAAAAAAAAAAAACAAACAAACAAACCCCCCCCCCGATATAGTTTTTGGTTCTGGATT 420
421 AGGTTTATTTGATCATAATTACATGCATCATTCTTTGATTACTATGAAGATTTTCTTAC 480
481 CAATTAATAATTCGAATTCATATCTCTTGATTATTAAATTAAATACGAGTGTGAATATCC 540
541 GTTTATCGATCACTCCAATCATGATTATGATTCTTGTGCTAATCCAGCAAATTATTAACA 600
601 AGAGTATTGAGAAAAAACCGAAAAATAAGAAAAGGGAAAGAGTAGTGACCCATGGAGTATG 660
661 TGAATAATTATCAAAGAGAATAAGAGATGACAACCAAAAGGTTGTGGAATAATGGTCCCT 720
721 GCCAGCTTTCTCTCACAATCAATATCGACCCTATTTGGATTTTCTGGATATTCGTAAAA 780
781 TTTGCGATAACGATTGTGAAAAATATTTTATTTGTTAGCTGATCTCAATATTATGTTCCA 840
841 GGTATTTGCATAATCTTCTGTTTAAAGCATATTTTGTCTTTCTTTTGTTCGTTTCTCT 900
901 TAACTATATATTATCGCGGATATATGATAACAATGATATATCACAAAACAATTGTCTGGG 960
961 ACCATTTTGAATAAACTTTTTCTCAAACATTACGGGACACTGGACTCGACCCTTAAATA 1020

FIG 10A



1021 CGATTTTACAGCGTCACTAGTTGAGATTACTAGCATAAAGCATAAAGGACCCGTTCAAGC 1080

1081 TATTTATACAAAGTTACAAACTGAATATAGCTTGAAATCCTTTAGAAAATTTTGGAATTA 1140

1141 CCGGTTGTTATGTAAATATAGATTTAGTGGTAAACAAATATGTTAATCAATTAGTGGTCA 1200

1201 ACATATACATAATTCCTTACAGAAAAACAACTTAAGAGAAGTTAACATATCCATATAT 1260

1261 GGGTATGCTATACCTTTCACGTATGCTATACTAGAGACTAAAGAATAGTTATGTGATGTC 1320

1321 GATAAATGAAATTCACACGCGTGGTAATAATTATGGGACCGTATGTTACGATCACTGCAA 1380

1381 ATATCATTCTTGGTTGGTCAACAATAAAAAACAAAAACAAGAAAAAAGAAAACGATTTTT 1440

1441 CTTGGATTCCATTCAATGATCTAAAATGCATAGATCTTTTGGGTTACAGTTTCGAAGTCC 1500

1501 TCTACAAGCGTGTAACCATCTGCAACTATTAAATTGCTTTCTTTAATGCATCTTTAACAT 1560

1561 ATTTATTGTTAGTTGGAATTTAATAAGAGCGAACTTGTAACATTACAATATTTATATTAG 1620

1621 ATA CTAGTATGTGATTATTCCAAATACATACTTTGGATGTTTAACTTAATCTTGTTTCT 1680

1681 TCCTACGGTATAAATATTAATCATCGAGGTAAAAAAGTTTTGTCTTATTTTCGCGATGC 1740

1741 ATGAAGGATAAACCTAATGACTTTAATTTTTTGAAAATGTAACCCCTTTTACTCATAGATT 1800

1801 AATTACCGTATGTTTTTGTGTCATAATGACAGCCTCTACAACTGTGATAGTCAATTTTT 1860

1861 TCTGCAAATATTAAATTAGGAATTCAATGCTACTATCAATAGAAGAAACAGCTGAGTATT 1920

1921 ACATTTTAATTTAAAGACAAAATTTTTGAAAAATGTTATAATTTCTAACAATATTATTAA 1980

1981 AATATGATGCCTATAATGTATTTCTATGTTCTTAAAAATTTTTTTTTTATTTTAGTTA 2040

2041 TAAATACATTATGAACCAATAATAGTTGGTGAATTCAAATATCTCCATTAATTTTTTTTG 2100

FIG 10B

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2101 AAATCTACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATT 2160
2161 TTGTTAACAGAACTTCCAAATTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAA 2220
2221 CTATTTTGTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATA 2280
2281 AGCCTATACGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGAT 2340
2341 TCAGAATTGGGACAACAATGAAAACGGAATTAATAATTAACCTTTAAAAATAAATAAAAAAT 2400
2401 TTGAGTAAATGTGTTTTCTGACTATTGAGGGGCAAAAAAAGACAATGCCAAAAGTCTAC 2460
2461 GGGTTTGACTGTCCAGTTCGGTAATAATCTAATAACTCTGTCTTTGACCGCACGCTCGTG 2520
2521 TAGGGGTCCTTCTGACATTTTCACTGTTCTACCCCTACTCGTGAGCCACCCCTTTTCCCA 2580
2581 TATCCTAAGGGTAATTTTGGAAATCCCAATTTAAACCGATTGAGACCGTACCGGACTTCC 2640
2641 TGGGATTCTGCTGGAGCATTTATCAAAAATTATTAGCACGAATGGGTTTATTAATTTAAA 2700
2701 AACTCACAACCTTGATCAGATAAAATTTTATAAACACTTTTACGATGGATTCTGATCGATCT 2760
2761 ATCTAATGACTTTTTTTTTTCTACCACGGTGGATGAAAGTTATAGTACTATTAGCCAGAG 2820
2821 ACAATTGATTATAGATATATCCATTAATCCATGATATTTATGATATAAATAGCTGTAAAA 2880
2881 CTATTTTCAGCATCGCAGCTTTCTGCAACTTTTGTTTTTAATTTAAGAGTTTAATAAATAA 2940
2941 AAGTATTAAGAGGAGCATAACGAGGCAACAAAAGTAATGAACACGGAGAAACAAAAGCCA 3000
3001 TGAAGCTCATTGGTTAGTTTAAGCTTAATAAGAAGATTTTATTAATTTTAATGACGATG 3060
3061 ATAACAATTATATTTTCTGACTTCTTTAAACCCCTCTTACAAACAGAAGCTCCCTTTT 3120
3121 TCAGTAGAAGTCCGATTCCCAATCTTAAAGACAAAGCCATTAGAAAGAGAAAGTGAGTGA 3180

FIG 10C

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3181 GAGAGAGAGAGAACTAGCTCCATGTTTCGAAACAGAGCATCATACTCTCTTACCTCTTCT 3240

exon 1

3241 TCTTCTCCCATCGCTTTTGTCTCTTCTCTTCTTCTTGAAGAGAAGAAATAG 3300

3301 AAAAACCAGATTCAATCTACCTCCGGGTAAATCCGGTTGGCCATTTCTTGGTGAAACCAT 3360

3361 CGGTTATCTTAAACCGTACACCGCCACAACACTCGGTGACTTCATGCAACAACATGTCTC 3420

3421 CAAGTAAACAACAACATCTTCCAAAACTCAAAAAATAAATCCTCTGTTTTTGAAATTT 3480

3481 GACTAATGTTGTTTATTTTACAGGTATGGTAAGATATATAGATCGAACTTGTTTGGAGAA 3540

exon 2

3541 CCAACGATCGTATCAGCTGATGCTGGACTTAATAGATTTCATATTACAAAACGAAGGAAGG 3600

3601 CTCTTTGAATGTAGTTATCCTAGAAGTATAGGTGGGATTCTTGGGAAATGGTCGATGCTT 3660

3661 GTTCTTGTTGGTGACATGCATAGAGATATGAGAAGTATCTCGCTTAACTTCTTAAGTCAC 3720

3721 GCACGTCTTAGAACTATTCTACTTAAAGATGTTGAGAGACATACTTTGTTTGTCTTGAT 3780

3781 TCTTGGCAACAAAACCTCTATTTTCTCTGCTCAAGACGAGGCCAAAAAGGTTTTTATTTTT 3840

3841 ATCTTTTATTTTGCTAAATTTTTTTGTTTATGAATCTTTAGAGTTTCTAACTTTTTTTTT 3900

3901 TTTAATTGAACAGTTTACGTTTAATCTAATGGCGAAGCATATAATGAGTATGGATCCTGG 3960

3961 AGAAGAAGAAACAGAGCAATTAAAGAAAGAGTATGTAACTTTCATGAAAGGAGTTGTCTC 4020

4021 TGCTCCTCTAAATCTACCAGGAACTGCTTATCATAAAGCTCTTCAGGTACATTTATTTTT 4080

4081 TTTTGCTGTAAAGTCACAACTCTCATTATAGGTTTTTAATTTTATTTTATGTGTAAAT 4140

4141 AAAATATCTAAAATGGTTGTGTAGTCACGAGCAACGATATTGAAGTTCATTGAGAGGAAA 4200

4201 ATGGAAGAGAGAAAATTGGATATCAAGGAAGAAGATCAAGAAGAAGAAGTGAAAACA 4260

FIG 10D

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261 GAGGATGAAGCAGAGATGAGTAAGAGTGATCATGTTAGGAAACAAAGAACAGACGATGAT 4320
4321 CTTTGGGATGGGTTTTGAAACATTCGAATTTATCGACGGAGCAAATTCTCGATCTCATT 4380
4381 CTTAGTTTGTTATTTGCCGGACATGAGAcTTCTTCTGTAGCCATTGCTCTCGCTATCTTC 4440
4441 TTCTTGCAAGCTTGCCCTAAAGCCGTTGAAGAGCTTAGGGTAAGATAATTATAACAGCAC 4500
4501 AAGTTAATTACTACCAAATTGTTACGTATTATATAAGTTATTATAGAATTATTCTATTAG 4560
4561 AATATACGATGAAAAAAGTATGTATATTTAATTGTCACATAATTTTATGTTTATTGATTTA 4620
4621 TACTTTTGAAGGAAGAGCATCTTGAGATCgCGAGGGCCAAGAAGGAACTAGGAGAGTCAG 4680
4681 AATTAAATTGGGATGATTACAAGAAAATGGACTTTACTCAATGTGTATGTTACTATCATT 4740
4741 CTCATTATTTATTCTATGTTTCATATGATTTATGATGAAACCAAATTATTGATTTTTTTT 4800
4801 TTGGTGTGTGTGAAGGTTATAAATGAACTCTTCGATTGGGAAATGTAGTTAGGTTTTTG 4860
4861 CATCGCAAAGCACTCAAAGATGTTCGGTACAAAGGTAAACTTTACGTACAAAATTTTAA 4920
4921 AATAATGAAATCCGGAATATTGAAATCTTATTGGATGAAAAATATTAATAATTACAT 4980
4981 TTCTTAATGTTGGAAAAAAGGATACGATATCCCTAGTGGGTGGAAAGTGTTACCGGTGAT 5040
5041 CTCAGCCGTACATTTGGATAATTCTCGTTATGACCAACCTAATCTCTTTAATCCTTGGAG 5100
5101 ATGGCAACAGGTAAATAAAAAGTTTCTCTCGTTAACTATCGAAAATTAGTGTATAGTTTT 5160
5161 TTCATCTATTGCATGAATAGATACGTCCTACGTGATTTACCTATCTATAGATACTATACG 5220
5221 AGAACTATTAATCTGGCAAAAACCTTTTATTATTATTATCTTTCAAGTTAGATCTTAACA 5280
5281 CGTCATGGATCATTGATCACATGAAAGCATATAAATTAATAAATAAGAGAGAGAAAGAGAC 5340

FIG 10E



5341 GTGTTGGTGTAAGTGTACGTGAAGACAATTAATTAGTAGGATGGTATGTCTTTAATGACG 5400
5401 TAGGAGCTGCCTAAATATTCTTATAATCGTGACCGTTGATTTATTATTAGTCACGGCTTT 5460
5461 GATACAATTTAAGATTTGACGGACGATGGTACCACGGCTTTGACGGATCTCACACGCCCG 5520
5521 ATGACTTGTACGTGCGTTAGATTCTGCCACGTTGACTGGTTTTAATACTTAGATTTATAA 5580
5581 CTCTATTAATTATAACAACATCAAAATCGGCGAATTAGAGAAATATACTATATAGTATTA 5640
5641 TTATGATTATTATGAGATAATACTTTATGAAATAAGATAATAATGGTAGTCATGATGTTA 5700
5701 TAGTGAGTGGGGAAGGTAAGAGGTGGTGAGAGATGATTAATGACCCACGTGGTGTGGTG 5760
5761 CCAACAAGCACGTGTTCTTCTTCCTTTTTTCTTCCCAACTTCTTTTTTTGGGGGTTTATT 5820
5821 GTGATTTATAAAATCGGTTTGTGCTTTTTTTTTGTGACGAGCAGCAAAACAACGGAGCGT 5880
exon 8
5881 CATCGTCAGGAAGTGGTAGTTTTTCGACGTGGGGAAACAACACTACATGCCGTTTGGAGGAG 5940
5941 GGCCAAGGCTATGTGCTGGTTCAGAGCTAGCCAAGTTAGAAATGGCAGTGTTTATTCATC 6000
6001 ATCTAGTTCTTAAATTCAATTGGGAATTAGCAGAAGATGATCAACCATTTCCTTTTCCTT 6060
6061 TTGTTGATTTTCCTAACGGTTTGCCTATTAGGGTTTCTCGTATTCTGTAAAAAAAAAAAAA 6120
6121 AGATGAAAGTATTTTTATTCTCTCTTTTTTTTTTGATAATTTAAATCATTTTTTTTGC 6180
6181 CCAATGATATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTTCGGG 6240
6241 TTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTT 6300
6301 GAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACTATTAAACCTT 6360
6361 AAATGGGCTTTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGACAACTTTTACT 6420

FIG 10F

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6421 TCGTTTTTGATCCGAAGCAATAACAAATTGTCAAATACCAAACACAAGAATTATGTAAAC 6480

6481 ACTCGTGTGTGTCTAGTGGGAAATCATTGGGCTGGAGACTGAACATCAGAACACAAGAAA 6540

6541 CCTGTCAATTATGGATACACCTCCTATGACGGTTTCCAACTTTATCTTGATTCTTATCG 6600

6601 TGTTACATTGACACAAAGAGTTAGGTGTCAAAAGGACTAAATGAATAACAATAGCTCTCA 6660

6661 GGATAAGAAGGTTCATAAAATGGTTTCTTTATTTTGAGAAGAAAGAGAGAGGAGCTTTTA 6720

6721 CTGTTTCTTGGGTCCTATTCCTTTAAATGAGAGGGTTTCGTTTTTACTTCTTCTATCTCA 6780

6781 TCATCTTTAGGATCCTCTTCTAGACGAGTAAAGTAATCCTCGTTACCAAGCAATGGTCTC 6840

6841 ATCTTTTGAAGACAGGTCTTTTCCAAGTCCTAGTTCAGGCCAAAGCTT 6888

FIG 10G

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FIG. 11

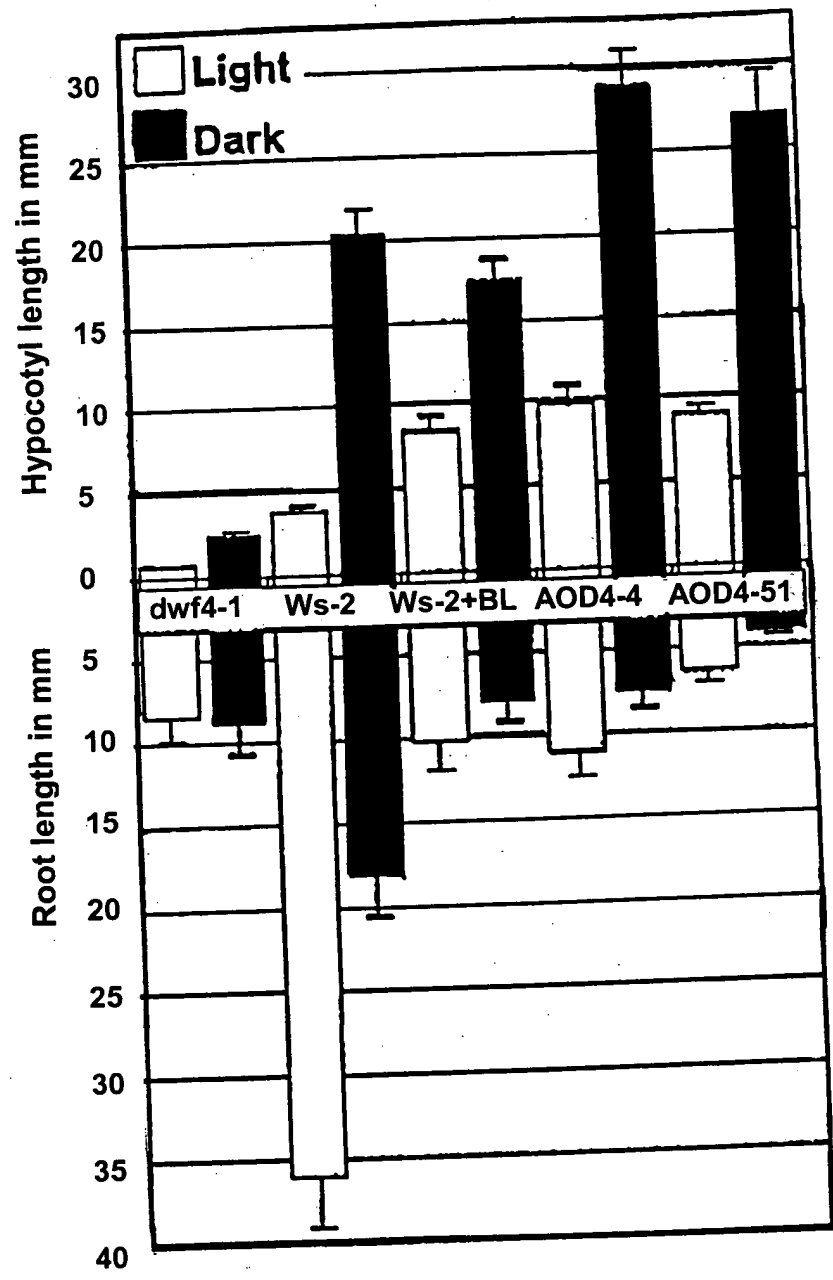


FIG. 12

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